

SEQUENCE LISTING

<110> Rory A.J. Curtis

<120> 55053, A Novel Human Eukaryotic Kinase  
and Uses Therefor

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Gln His Ala Gln Tyr Val Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly
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cac aga gac cta aag ccc gag aac ctg ctt ttg gat gag aaa aac aac His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn 155 160 165	592
atc cgc att gca gac ttc ggc atg gcg tcc ctg cag gtg ggg gac agc Ile Arg Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser 170 175 180 185	640
ctc ctg gag acc agc tgc ggg tcc ccc cat tat gcg tgt cca gag gtg Leu Leu Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val 190 195 200	688
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Lys His Glu Pro Asp Pro Cys Leu Glu Pro Ala Pro Gly Arg Arg Val
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Pro Met Leu Ser Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met
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Pro	Glu	Leu	Ser	Ser	Ser	Pro	Arg	Arg	Gly	Pro	Pro	Lys	Asp	Lys	Lys
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Ala Gly Ala Pro Pro Arg Ser Leu Gln Pro Pro Pro Gly Arg Pro Asp
      740              745              750

cca gag ctg agc agc tct ccc cgc cga ggc ccc ccc aag gac aag aag 2304
Pro Glu Leu Ser Ser Ser Pro Arg Arg Gly Pro Pro Lys Asp Lys Lys
      755              760              765

ctc ctg gcc acc aac ggg acc cct ctg ccc 2334
Leu Leu Ala Thr Asn Gly Thr Pro Leu Pro
      770              775

```

```

<210> 4
<211> 13
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> serine/threonine kinase signature motif consensus
sequence

```

```

<221> VARIANT
<222> 1
<223> Xaa= Leu, Ile, Val, Met, Phe, Tyr, or Cys

```

```

<221> VARIANT
<222> 2, 4, 8, 9
<223> Xaa=any amino acids

```

```

<221> VARIANT
<222> 3
<223> Xaa= His or Tyr

```

```

<221> VARIANT
<222> 6
<223> Xaa= Leu, Ile, Val, Met, Phe, or Tyr

```

```

<221> VARIANT
<222> 11, 12, 13
<223> Xaa= Leu, Ile, Val, Met, Phe, Tyr, Cys, or Thr

```

```

<400> 4
Xaa Xaa Xaa Xaa Asp Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa
 1             5             10

```

```

<210> 5
<211> 278
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Eukaryotic protein kinase domain

```

```

<400> 5
Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
 1             5             10             15
Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
      20             25             30

```

- 11 -

Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser  
                   35                  40                  45  
 His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp  
                   50                  55                  60  
 His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Asp Leu Phe Asp  
                   65                  70                  75                  80  
 Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile  
                   85                  90                  95  
 Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile  
                   100                  105                  110  
 Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly  
                   115                  120                  125  
 Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu  
                   130                  135                  140  
 Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile  
                   145                  150                  155                  160  
 Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly  
                   165                  170                  175  
 Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala  
                   180                  185                  190  
 Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile  
                   195                  200                  205  
 Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile  
                   210                  215                  220  
 Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu  
                   225                  230                  235                  240  
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu  
                   245                  250                  255  
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile  
                   260                  265                  270  
 Leu Asn His Pro Trp Phe  
                   275

<210> 6  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UBA domain

<400> 6  
 Glu Asp Glu Glu Lys Ile Glu Gln Leu Val Glu Met Gly Phe Asp Arg  
                   1                  5                  10                  15  
 Glu Glu Val Val Lys Ala Leu Arg Ala Thr Asn Gly Asn Gly Val Glu  
                   20                  25                  30  
 Arg Ala Ala Glu Trp Leu Leu Ser His  
                   35                  40

<210> 7  
 <211> 231  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> serkin\_6 domain

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&lt;400&gt; 7

```

Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
 1          5          10          15
Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
 20          25          30
Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
 35          40          45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
 50          55          60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Phe Asp Leu Leu
 65          70          75          80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
 85          90          95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
100          105          110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
115          120          125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
130          135          140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145          150          155          160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
165          170          175
Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
180          185          190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
195          200          205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
210          215          220
Ile Lys Ala His Pro Phe Phe
225          230

```

&lt;210&gt; 8

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; tyrkin\_6 domain

&lt;400&gt; 8

```

Leu Thr Leu Gly Lys Lys Leu Gly Glu Gly Ala Phe Gly Glu Val Tyr
 1          5          10          15
Lys Gly Thr Leu Lys Ile Glu Val Ala Val Lys Thr Leu Lys Glu Asp
 20          25          30
Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
 35          40          45
Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
 50          55          60
Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
 65          70          75          80
Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
 85          90          95
Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
100          105          110
Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
115          120          125
Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
130          135          140

```

Gly	Leu	Ser	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Lys	Lys	Gly	Glu	Ser	Lys
145				150						155					160
Asp	Tyr	Tyr	Arg	Lys	Lys	Gly	Gly	Lys	Gly	Gly	Lys	Thr	Leu	Leu	Pro
				165					170					175	
Ile	Arg	Trp	Met	Ala	Pro	Glu	Ser	Leu	Lys	Asp	Gly	Lys	Phe	Thr	Ser
			180					185					190		
Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Thr
			195				200					205			
Leu	Gly	Glu	Gln	Pro	Tyr	Pro	Gly	Glu	Ile	Gln	Gln	Phe	Met	Ser	Asn
						215					220				
Glu	Glu	Val	Leu	Glu	Tyr	Leu	Lys	Lys	Gly	Tyr	Arg	Leu	Pro	Lys	Pro
225					230					235					240
Glu	Asn	Asp	Leu	Pro	Ile	Ser	Ser	Val	Thr	Cys	Pro	Asp	Glu	Leu	Tyr
				245					250					255	
Asp	Leu	Met	Leu	Gln	Cys	Trp	Ala	Glu	Asp	Pro	Glu	Asp	Arg	Pro	Thr
			260					265					270		
Phe	Ser	Glu	Leu	Val	Glu	Arg	Leu								
			275				280								